

Replace the paragraph beginning at page 15, line 1, with the following rewritten paragraph:

a² --Figure 1B depicts the predicted amino acid sequence of Daedalos (Daed; SEQ ID NO:1), aligned with the other Ikaros gene family members, Helios (Hel; SEQ ID NO:2), Aiolos (Aio; SEQ ID NO:3), and Ikaros (Ik; SEQ ID NO:4). Residues conserved in Ikaros family members are highlighted in gray and the zinc finger domains are boxed.--

Replace the paragraph beginning at page 15, line 5, with the following rewritten paragraph:

a³ --Figure 1C depicts the amino acid sequence of the Xenopus Daedalos (xDaed; SEQ ID NO:5) protein, aligned with the amino acid sequence of the mouse Daedalos (mDaed) protein (SEQ ID NO:1).--

Replace the paragraph beginning at page 16, line 15, with the following rewritten paragraph:

a⁴ --A fourth member of the Ikaros gene family, designated Daedalos, was cloned using PCR with degenerate primers (Morgan et al. (1997) EMBO J 16:2004; Honma et al. (1999) FEBS Letters 447:76). PCR amplification was performed as follows. 40 cycles (95°, 30 seconds; 45°, 1.5 minutes; 72°, 2 minutes) were carried out in a Pfu buffer containing 3 mM MgSO₄, using degenerate primers designed from conserved regions of the murine Ikaros family of proteins: DEG 10 (TG (T/C)AA(T/C)CA(A/G)TG(T/C)GGIGCI (T/A)CITT(T/C)AC; SEQ ID NO:6) and DEG 12 (TG(G/A)CAICCCAT(G/A)TGIATIGT (G/A)(T/A)ACAT; SEQ ID NO:7). This resulted in the amplification of a 900 base pair product. 3'and 5' RACE (Marathon, Promega) were employed to clone the remaining coding sequences for each transcript as well as the 5'and 3' UTRs.--

Replace the paragraph beginning at page 19, line 3, with the following rewritten paragraph:

ds
--PCR analysis of Daedalus transcripts confirmed that they are expressed from stage 11 while primary neurogenesis is occurring. Total RNA was prepared from 100 *Xenopus laevis* embryos at stage 11 or 12 and 2 micrograms were reverse transcribed. 165 nanograms of cDNA products (16.5 ng for histone H-4) were amplified in the presence of 1.5 μ Ci each of [P32] dATP and [P32] dCTP using the following primer pairs: histone H-4 (20 cycles, using primers 5'-AGGGACAACATCCAGGGCATCACC (SEQ ID NO:8) and 3'-ATCCATGGCGGTAACGGTCTTCCT (SEQ ID NO:9)); XDaedalus (31 cycles, using primers 5'-ATTCTGTAAC TACGCTTGTCGTCG (SEQ ID NO:10) and 3'-AACAATIGCCATAAGCAGTGTCCA (SEQ ID NO:11)); and neurogenin-1b (28 cycles, using primers 5'-CATATTGGTACAGGACTCCTATCC (SEQ ID NO:12) and 3'-CTTGACCCTTATGGGAAGCAGGAA (SEQ ID NO:13)). The number of cycles employed were in the range for linear amplification of each target. The products were separated on a 5% polyacrylamide gel and quantitated on a phosphorimager (Molecular Dynamics). Input cDNA levels were corrected to achieve similar histone H-4 content.--